

SEQUENCE LISTING

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 The Regents of the University of California
 The Government of the United States of America
 as represented by the Secretary of the
 Department of Health and Human Services

<120> Mammalian Sweet Taste Receptors

<130> 02307E-120110US

<140> US 09/927,315
 <141> 2001-08-10

<150> US 60/302,898
 <151> 2001-07-03

<160> 25

<170> PatentIn Ver. 2.1

<210> 1
 <211> 840
 <212> PRT
 <213> Rattus sp.

<220>
 <223> rat T1R1 sweet taste receptor

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 Cys Trp Ala Phe Ser Cys Gln Arg Thr Glu Ser Ser Pro Gly Phe Ser
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 Leu Pro Gly Asp Phe Leu Leu Ala Gly Leu Phe Ser Leu His Gly Asp
 35 40 45
 Cys Leu Gln Val Arg His Arg Pro Leu Val Thr Ser Cys Asp Arg Pro
 50 55 60
 Asp Ser Phe Asn Gly His Gly Tyr His Leu Phe Gln Ala Met Arg Phe
 65 70 75 80
 Thr Val Glu Glu Ile Asn Asn Ser Ser Ala Leu Leu Pro Asn Ile Thr
 85 90 95
 Leu Gly Tyr Glu Leu Tyr Asp Val Cys Ser Glu Ser Ala Asn Val Tyr
 100 105 110
 Ala Thr Leu Arg Val Leu Ala Leu Gln Gly Pro Arg His Ile Glu Ile
 115 120 125

Gln Lys Asp Leu Arg Asn His Ser Ser Lys Val Val Ala Phe Ile Gly
 130 135 140
 Pro Asp Asn Thr Asp His Ala Val Thr Thr Ala Ala Leu Leu Gly Pro
 145 150 155 160
 Phe Leu Met Pro Leu Val Ser Tyr Glu Ala Ser Ser Val Val Leu Ser
 165 170 175
 Ala Lys Arg Lys Phe Pro Ser Phe Leu Arg Thr Val Pro Ser Asp Arg
 180 185 190
 His Gln Val Glu Val Met Val Gln Leu Leu Gln Ser Phe Gly Trp Val
 195 200 205
 Trp Ile Ser Leu Ile Gly Ser Tyr Gly Asp Tyr Gly Gln Leu Gly Val
 210 215 220
 Gln Ala Leu Glu Glu Leu Ala Val Pro Arg Gly Ile Cys Val Ala Phe
 225 230 235 240
 Lys Asp Ile Val Pro Phe Ser Ala Arg Val Gly Asp Pro Arg Met Gln
 245 250 255
 Ser Met Met Gln His Leu Ala Gln Ala Arg Thr Thr Val Val Val Val
 260 265 270
 Phe Ser Asn Arg His Leu Ala Arg Val Phe Phe Arg Ser Val Val Leu
 275 280 285
 Ala Asn Leu Thr Gly Lys Val Trp Val Ala Ser Glu Asp Trp Ala Ile
 290 295 300
 Ser Thr Tyr Ile Thr Ser Val Thr Gly Ile Gln Gly Ile Gly Thr Val
 305 310 315 320
 Leu Gly Val Ala Val Gln Gln Arg Gln Val Pro Gly Leu Lys Glu Phe
 325 330 335
 Glu Glu Ser Tyr Val Arg Ala Val Thr Ala Ala Pro Ser Ala Cys Pro
 340 345 350
 Glu Gly Ser Trp Cys Ser Thr Asn Gln Leu Cys Arg Glu Cys His Thr
 355 360 365
 Phe Thr Thr Arg Asn Met Pro Thr Leu Gly Ala Phe Ser Met Ser Ala
 370 375 380
 Ala Tyr Arg Val Tyr Glu Ala Val Tyr Ala Val Ala His Gly Leu His
 385 390 395 400
 Gln Leu Leu Gly Cys Thr Ser Glu Ile Cys Ser Arg Gly Pro Val Tyr
 405 410 415
 Pro Trp Gln Leu Leu Gln Gln Ile Tyr Lys Val Asn Phe Leu Leu His
 420 425 430
 Glu Asn Thr Val Ala Phe Asp Asp Asn Gly Asp Thr Leu Gly Tyr Tyr
 435 440 445

Asp Ile Ile Ala Trp Asp Trp Asn Gly Pro Glu Trp Thr Phe Glu Ile
 450 455 460
 Ile Gly Ser Ala Ser Leu Ser Pro Val His Leu Asp Ile Asn Lys Thr
 465 470 475 480
 Lys Ile Gln Trp His Gly Lys Asn Asn Gln Val Pro Val Ser Val Cys
 485 490 495
 Thr Thr Asp Cys Leu Ala Gly His His Arg Val Val Val Gly Ser His
 500 505 510
 His Cys Cys Phe Glu Cys Val Pro Cys Glu Ala Gly Thr Phe Leu Asn
 515 520 525
 Met Ser Glu Leu His Ile Cys Gln Pro Cys Gly Thr Glu Glu Trp Ala
 530 535 540
 Pro Lys Glu Ser Thr Thr Cys Phe Pro Arg Thr Val Glu Phe Leu Ala
 545 550 555 560
 Trp His Glu Pro Ile Ser Leu Val Leu Ile Ala Ala Asn Thr Leu Leu
 565 570 575
 Leu Leu Leu Leu Val Gly Thr Ala Gly Leu Phe Ala Trp His Phe His
 580 585 590
 Thr Pro Val Val Arg Ser Ala Gly Gly Arg Leu Cys Phe Leu Met Leu
 595 600 605
 Gly Ser Leu Val Ala Gly Ser Cys Ser Phe Tyr Ser Phe Phe Gly Glu
 610 615 620
 Pro Thr Val Pro Ala Cys Leu Leu Arg Gln Pro Leu Phe Ser Leu Gly
 625 630 635 640
 Phe Ala Ile Phe Leu Ser Cys Leu Thr Ile Arg Ser Phe Gln Leu Val
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 Ile Ile Phe Lys Phe Ser Thr Lys Val Pro Thr Phe Tyr Arg Thr Trp
 660 665 670
 Ala Gln Asn His Gly Ala Gly Leu Phe Val Ile Val Ser Ser Thr Val
 675 680 685
 His Leu Leu Ile Cys Leu Thr Trp Leu Val Met Trp Thr Pro Arg Pro
 690 695 700
 Thr Arg Glu Tyr Gln Arg Phe Pro His Leu Val Ile Leu Glu Cys Thr
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 Glu Val Asn Ser Val Gly Phe Leu Leu Ala Phe Thr His Asn Ile Leu
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 Leu Ser Ile Ser Thr Phe Val Cys Ser Tyr Leu Gly Lys Glu Leu Pro
 740 745 750
 Glu Asn Tyr Asn Glu Ala Lys Cys Val Thr Phe Ser Leu Leu Leu Asn
 755 760 765

Phe Val Ser Trp Ile Ala Phe Phe Thr Met Ala Ser Ile Tyr Gln Gly
 770 775 780
 Ser Tyr Leu Pro Ala Val Asn Val Leu Ala Gly Leu Thr Thr Leu Ser
 785 790 795 800
 Gly Gly Phe Ser Gly Tyr Phe Leu Pro Lys Cys Tyr Val Ile Leu Cys
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 Tyr Thr Arg Arg Cys Gly Thr Thr
 835 840

<210> 2
 <211> 842
 <212> PRT
 <213> Mus musculus

<220>
 <223> mouse T1R1 sweet taste receptor

<400> 2
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 Phe Ser Leu Pro Gly Asp Phe Leu Leu Ala Gly Leu Phe Ser Leu His
 35 40 45
 Ala Asp Cys Leu Gln Val Arg His Arg Pro Leu Val Thr Ser Cys Asp
 50 55 60
 Arg Ser Asp Ser Phe Asn Gly His Gly Tyr His Leu Phe Gln Ala Met
 65 70 75 80
 Arg Phe Thr Val Glu Glu Ile Asn Asn Ser Thr Ala Leu Leu Pro Asn
 85 90 95
 Ile Thr Leu Gly Tyr Glu Leu Tyr Asp Val Cys Ser Glu Ser Ser Asn
 100 105 110
 Val Tyr Ala Thr Leu Arg Val Pro Ala Gln Gln Gly Thr Gly His Leu
 115 120 125
 Glu Met Gln Arg Asp Leu Arg Asn His Ser Ser Lys Val Val Ala Leu
 130 135 140
 Ile Gly Pro Asp Asn Thr Asp His Ala Val Thr Thr Ala Ala Leu Leu
 145 150 155 160
 Ser Pro Phe Leu Met Pro Leu Val Ser Tyr Glu Ala Ser Ser Val Ile
 165 170 175
 Leu Ser Gly Lys Arg Lys Phe Pro Ser Phe Leu Arg Thr Ile Pro Ser
 180 185 190

Asp Lys Tyr Gln Val Glu Val Ile Val Arg Leu Leu Gln Ser Phe Gly
 195 200 205
 Trp Val Trp Ile Ser Leu Val Gly Ser Tyr Gly Asp Tyr Gly Gln Leu
 210 215 220
 Gly Val Gln Ala Leu Glu Glu Leu Ala Thr Pro Arg Gly Ile Cys Val
 225 230 235 240
 Ala Phe Lys Asp Val Val Pro Leu Ser Ala Gln Ala Gly Asp Pro Arg
 245 250 255
 Met Gln Arg Met Met Leu Arg Leu Ala Arg Ala Arg Thr Thr Val Val
 260 265 270
 Val Val Phe Ser Asn Arg His Leu Ala Gly Val Phe Phe Arg Ser Val
 275 280 285
 Val Leu Ala Asn Leu Thr Gly Lys Val Trp Ile Ala Ser Glu Asp Trp
 290 295 300
 Ala Ile Ser Thr Tyr Ile Thr Asn Val Pro Gly Ile Gln Gly Ile Gly
 305 310 315 320
 Thr Val Leu Gly Val Ala Ile Gln Gln Arg Gln Val Pro Gly Leu Lys
 325 330 335
 Glu Phe Glu Glu Ser Tyr Val Gln Ala Val Met Gly Ala Pro Arg Thr
 340 345 350
 Cys Pro Glu Gly Ser Trp Cys Gly Thr Asn Gln Leu Cys Arg Glu Cys
 355 360 365
 His Ala Phe Thr Thr Trp Asn Met Pro Glu Leu Gly Ala Phe Ser Met
 370 375 380
 Ser Ala Ala Tyr Asn Val Tyr Glu Ala Val Tyr Ala Val Ala His Gly
 385 390 395 400
 Leu His Gln Leu Leu Gly Cys Thr Ser Gly Thr Cys Ala Arg Gly Pro
 405 410 415
 Val Tyr Pro Trp Gln Leu Leu Gln Gln Ile Tyr Lys Val Asn Phe Leu
 420 425 430
 Leu His Lys Lys Thr Val Ala Phe Asp Asp Lys Gly Asp Pro Leu Gly
 435 440 445
 Tyr Tyr Asp Ile Ile Ala Trp Asp Trp Asn Gly Pro Glu Trp Thr Phe
 450 455 460
 Glu Val Ile Gly Ser Ala Ser Leu Ser Pro Val His Leu Asp Ile Asn
 465 470 475 480
 Lys Thr Lys Ile Gln Trp His Gly Lys Asn Asn Gln Val Pro Val Ser
 485 490 495
 Val Cys Thr Arg Asp Cys Leu Glu Gly His His Arg Leu Val Met Gly
 500 505 510

Ser	His	His	Cys	Cys	Phe	Glu	Cys	Met	Pro	Cys	Glu	Ala	Gly	Thr	Phe		
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Leu	Asn	Thr	Ser	Glu	Leu	His	Thr	Cys	Gln	Pro	Cys	Gly	Thr	Glu	Glu		
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Leu	Val	Ile	Ile	Phe	Lys	Phe	Ser	Thr	Lys	Val	Pro	Thr	Phe	Tyr	His		
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Thr	Trp	Ala	Gln	Asn	His	Gly	Ala	Gly	Ile	Phe	Val	Ile	Val	Ser	Ser		
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Arg	Pro	Thr	Arg	Glu	Tyr	Gln	Arg	Phe	Pro	His	Leu	Val	Ile	Leu	Glu		
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Cys	Thr	Glu	Val	Asn	Ser	Val	Gly	Phe	Leu	Val	Ala	Phe	Ala	His	Asn		
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Ile	Leu	Leu	Ser	Ile	Ser	Thr	Phe	Val	Cys	Ser	Tyr	Leu	Gly	Lys	Glu		
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Leu	Pro	Glu	Asn	Tyr	Asn	Glu	Ala	Lys	Cys	Val	Thr	Phe	Ser	Leu	Leu		
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Leu	His	Phe	Val	Ser	Trp	Ile	Ala	Phe	Phe	Thr	Met	Ser	Ser	Ile	Tyr		
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Gln	Gly	Ser	Tyr	Leu	Pro	Ala	Val	Asn	Val	Leu	Ala	Gly	Leu	Ala	Thr		
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Leu	Ser	Gly	Gly	Phe	Ser	Gly	Tyr	Phe	Leu	Pro	Lys	Cys	Tyr	Val	Ile		
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Leu	Cys	Arg	Pro	Glu	Leu	Asn	Asn	Thr	Glu	His	Phe	Gln	Ala	Ser	Ile		
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Gln Asp Tyr Thr Arg Arg Cys Gly Thr Thr
 835 840

<210> 3
 <211> 777
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human T1R1 sweet taste receptor

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 Arg Leu Gly Val Glu Glu Ile Asn Asn Ser Thr Ala Leu Leu Pro Asn
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 Ile Thr Leu Gly Tyr Gln Leu Tyr Asp Val Cys Ser Asp Ser Ala Asn
 35 40 45
 Val Tyr Ala Thr Leu Arg Val Leu Ser Leu Pro Gly Gln His His Ile
 50 55 60
 Glu Leu Gln Gly Asp Leu Leu His Tyr Ser Pro Thr Val Leu Ala Val
 65 70 75 80
 Ile Gly Pro Asp Ser Thr Asn Arg Ala Ala Thr Thr Ala Ala Leu Leu
 85 90 95
 Ser Pro Phe Leu Val His Ile Ser Tyr Ala Ala Ser Ser Glu Thr Leu
 100 105 110
 Ser Val Lys Arg Gln Tyr Pro Ser Phe Leu Arg Thr Ile Pro Asn Asp
 115 120 125
 Lys Tyr Gln Val Glu Thr Met Val Leu Leu Leu Gln Lys Phe Gly Trp
 130 135 140
 Thr Trp Ile Ser Leu Val Gly Ser Ser Asp Asp Tyr Gly Gln Leu Gly
 145 150 155 160
 Val Gln Ala Leu Glu Asn Gln Ala Leu Val Arg Gly Ile Cys Ile Ala
 165 170 175
 Phe Lys Asp Ile Met Pro Phe Ser Ala Gln Val Gly Asp Glu Arg Met
 180 185 190
 Gln Cys Leu Met Arg His Leu Ala Gln Ala Gly Ala Thr Val Val Val
 195 200 205
 Val Phe Ser Ser Arg Gln Leu Ala Arg Val Phe Phe Glu Ser Val Val
 210 215 220
 Leu Thr Asn Leu Thr Gly Lys Val Trp Val Ala Ser Glu Ala Trp Ala
 225 230 235 240
 Leu Ser Arg His Ile Thr Gly Val Pro Gly Ile Gln Arg Ile Gly Met
 245 250 255

Val Leu Gly Val Ala Ile Gln Lys Arg Ala Val Pro Gly Leu Lys Ala
 260 265 270
 Phe Glu Glu Ala Tyr Ala Arg Ala Asp Lys Glu Ala Pro Arg Pro Cys
 275 280 285
 His Lys Gly Ser Trp Cys Ser Ser Asn Gln Leu Cys Arg Glu Cys Gln
 290 295 300
 Ala Phe Met Ala His Thr Met Pro Lys Leu Lys Ala Phe Ser Met Ser
 305 310 315 320
 Ser Ala Tyr Asn Ala Tyr Arg Ala Val Tyr Ala Val Ala His Gly Leu
 325 330 335
 His Gln Leu Leu Gly Cys Ala Ser Glu Leu Cys Ser Arg Gly Arg Val
 340 345 350
 Tyr Pro Trp Gln Leu Leu Glu Gln Ile His Lys Val His Phe Leu Leu
 355 360 365
 His Lys Asp Thr Val Ala Phe Asn Asp Asn Arg Asp Pro Leu Ser Ser
 370 375 380
 Tyr Asn Ile Ile Ala Trp Asp Trp Asn Gly Pro Lys Trp Thr Phe Thr
 385 390 395 400
 Val Leu Gly Ser Ser Thr Trp Ser Pro Val Gln Leu Asn Ile Asn Glu
 405 410 415
 Thr Lys Ile Gln Trp His Gly Lys Asn His Gln Val Pro Lys Ser Val
 420 425 430
 Cys Ser Ser Asp Cys Leu Glu Gly His Gln Arg Val Val Thr Gly Phe
 435 440 445
 His His Cys Cys Phe Glu Cys Val Pro Cys Gly Ala Gly Thr Phe Leu
 450 455 460
 Asn Lys Ser Glu Leu Tyr Arg Cys Gln Pro Cys Gly Thr Glu Glu Trp
 465 470 475 480
 Ala Pro Glu Gly Ser Gln Thr Cys Phe Pro Arg Thr Val Val Phe Leu
 485 490 495
 Ala Leu Arg Glu His Thr Ser Trp Val Leu Leu Ala Ala Asn Thr Leu
 500 505 510
 Leu Leu Leu Leu Leu Leu Gly Thr Ala Gly Leu Phe Ala Trp His Leu
 515 520 525
 Asp Thr Pro Val Val Arg Ser Ala Gly Gly Arg Leu Cys Phe Leu Met
 530 535 540
 Leu Gly Ser Leu Ala Ala Gly Ser Gly Ser Leu Tyr Gly Phe Phe Gly
 545 550 555 560
 Glu Pro Thr Arg Pro Ala Cys Leu Leu Arg Gln Ala Leu Phe Ala Leu
 565 570 575

Gly Phe Thr Ile Phe Leu Ser Cys Leu Thr Val Arg Ser Phe Gln Leu
 580 585 590
 Ile Ile Ile Phe Lys Phe Ser Thr Lys Val Pro Thr Phe Tyr His Ala
 595 600 605
 Trp Val Gln Asn His Gly Ala Gly Leu Phe Val Met Ile Ser Ser Ala
 610 615 620
 Ala Gln Leu Leu Ile Cys Leu Thr Trp Leu Val Val Trp Thr Pro Leu
 625 630 635 640
 Pro Ala Arg Glu Tyr Gln Arg Phe Pro His Leu Val Met Leu Glu Cys
 645 650 655
 Thr Glu Thr Asn Ser Leu Gly Phe Ile Leu Ala Phe Leu Tyr Asn Gly
 660 665 670
 Leu Leu Ser Ile Ser Ala Phe Ala Cys Ser Tyr Leu Gly Lys Asp Leu
 675 680 685
 Pro Glu Asn Tyr Asn Glu Ala Lys Cys Val Thr Phe Ser Leu Leu Phe
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 Asn Phe Val Ser Trp Ile Ala Phe Phe Thr Thr Ala Ser Val Tyr Asp
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 Gly Lys Tyr Leu Pro Ala Ala Asn Met Met Ala Gly Leu Ser Ser Leu
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 Ser Ser Gly Phe Gly Gly Tyr Phe Leu Pro Lys Cys Tyr Val Ile Leu
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 Cys Arg Pro Asp Leu Asn Ser Thr Glu His Phe Gln Ala Ser Ile Gln
 755 760 765
 Asp Tyr Thr Arg Arg Cys Gly Ser Thr
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<210> 4

<211> 2771

<212> DNA

<213> Rattus sp.

<220>

<223> rat T1R1 sweet taste receptor

<400> 4

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<210> 5

<211> 2579

<212> DNA

<213> Mus musculus

<220>

<223> mouse T1R1 sweet taste receptor

<400> 5

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<210> 6

<211> 2333

<212> DNA

<213> Homo sapiens

<220>

<223> human T1R1 sweet taste receptor

<400> 6

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<210> 7
 <211> 843
 <212> PRT
 <213> Rattus sp.

<220>
 <223> rat T1R2 sweet taste receptor

<400> 7
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 Val Leu Pro Lys Pro Gly Lys Leu Val Glu Asn Ser Asp Phe His Leu
 20 25 30
 Ala Gly Asp Tyr Leu Leu Gly Gly Leu Phe Thr Leu His Ala Asn Val
 35 40 45
 Lys Ser Ile Ser His Leu Ser Tyr Leu Gln Val Pro Lys Cys Asn Glu
 50 55 60
 Phe Thr Met Lys Val Leu Gly Tyr Asn Leu Met Gln Ala Met Arg Phe
 65 70 75 80
 Ala Val Glu Glu Ile Asn Asn Cys Ser Ser Leu Leu Pro Gly Val Leu
 85 90 95
 Leu Gly Tyr Glu Met Val Asp Val Cys Tyr Leu Ser Asn Asn Ile His
 100 105 110
 Pro Gly Leu Tyr Phe Leu Ala Gln Asp Asp Asp Leu Leu Pro Ile Leu
 115 120 125
 Lys Asp Tyr Ser Gln Tyr Met Pro His Val Val Ala Val Ile Gly Pro
 130 135 140
 Asp Asn Ser Glu Ser Ala Ile Thr Val Ser Asn Ile Leu Ser His Phe
 145 150 155 160
 Leu Ile Pro Gln Ile Thr Tyr Ser Ala Ile Ser Asp Lys Leu Arg Asp
 165 170 175

Lys	Arg	His	Phe	Pro	Ser	Met	Leu	Arg	Thr	Val	Pro	Ser	Ala	Thr	His		
			180					185					190				
His	Ile	Glu	Ala	Met	Val	Gln	Leu	Met	Val	His	Phe	Gln	Trp	Asn	Trp		
		195					200					205					
Ile	Val	Val	Leu	Val	Ser	Asp	Asp	Asp	Tyr	Gly	Arg	Glu	Asn	Ser	His		
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Leu	Leu	Ser	Gln	Arg	Leu	Thr	Lys	Thr	Ser	Asp	Ile	Cys	Ile	Ala	Phe		
225					230					235					240		
Gln	Glu	Val	Leu	Pro	Ile	Pro	Glu	Ser	Ser	Gln	Val	Met	Arg	Ser	Glu		
				245					250					255			
Glu	Gln	Arg	Gln	Leu	Asp	Asn	Ile	Leu	Asp	Lys	Leu	Arg	Arg	Thr	Ser		
			260					265						270			
Ala	Arg	Val	Val	Val	Val	Phe	Ser	Pro	Glu	Leu	Ser	Leu	Tyr	Ser	Phe		
		275					280					285					
Phe	His	Glu	Val	Leu	Arg	Trp	Asn	Phe	Thr	Gly	Phe	Val	Trp	Ile	Ala		
	290					295					300						
Ser	Glu	Ser	Trp	Ala	Ile	Asp	Pro	Val	Leu	His	Asn	Leu	Thr	Glu	Leu		
305					310					315					320		
Arg	His	Thr	Gly	Thr	Phe	Leu	Gly	Val	Thr	Ile	Gln	Arg	Val	Ser	Ile		
			325						330					335			
Pro	Gly	Phe	Ser	Gln	Phe	Arg	Val	Arg	Arg	Asp	Lys	Pro	Gly	Tyr	Pro		
			340					345					350				
Val	Pro	Asn	Thr	Thr	Asn	Leu	Arg	Thr	Thr	Cys	Asn	Gln	Asp	Cys	Asp		
		355					360					365					
Ala	Cys	Leu	Asn	Thr	Thr	Lys	Ser	Phe	Asn	Asn	Ile	Leu	Ile	Leu	Ser		
	370					375					380						
Gly	Glu	Arg	Val	Val	Tyr	Ser	Val	Tyr	Ser	Ala	Val	Tyr	Ala	Val	Ala		
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His	Ala	Leu	His	Arg	Leu	Leu	Gly	Cys	Asn	Arg	Val	Arg	Cys	Thr	Lys		
				405					410					415			
Gln	Lys	Val	Tyr	Pro	Trp	Gln	Leu	Leu	Arg	Glu	Ile	Trp	His	Val	Asn		
		420					425						430				
Phe	Thr	Leu	Leu	Gly	Asn	Arg	Leu	Phe	Phe	Asp	Gln	Gln	Gly	Asp	Met		
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Pro	Met	Leu	Leu	Asp	Ile	Ile	Gln	Trp	Gln	Trp	Asp	Leu	Ser	Gln	Asn		
	450					455					460						
Pro	Phe	Gln	Ser	Ile	Ala	Ser	Tyr	Ser	Pro	Thr	Ser	Lys	Arg	Leu	Thr		
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Tyr	Ile	Asn	Asn	Val	Ser	Trp	Tyr	Thr	Pro	Asn	Asn	Thr	Val	Pro	Val		
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Ser Met Cys Ser Lys Ser Cys Gln Pro Gly Gln Met Lys Lys Ser Val
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 Gly Leu His Pro Cys Cys Phe Glu Cys Leu Asp Cys Met Pro Gly Thr
 515 520 525
 Tyr Leu Asn Arg Ser Ala Asp Glu Phe Asn Cys Leu Ser Cys Pro Gly
 530 535 540
 Ser Met Trp Ser Tyr Lys Asn Asp Ile Thr Cys Phe Gln Arg Arg Pro
 545 550 555 560
 Thr Phe Leu Glu Trp His Glu Val Pro Thr Ile Val Val Ala Ile Leu
 565 570 575
 Ala Ala Leu Gly Phe Phe Ser Thr Leu Ala Ile Leu Phe Ile Phe Trp
 580 585 590
 Arg His Phe Gln Thr Pro Met Val Arg Ser Ala Gly Gly Pro Met Cys
 595 600 605
 Phe Leu Met Leu Val Pro Leu Leu Leu Ala Phe Gly Met Val Pro Val
 610 615 620
 Tyr Val Gly Pro Pro Thr Val Phe Ser Cys Phe Cys Arg Gln Ala Phe
 625 630 635 640
 Phe Thr Val Cys Phe Ser Ile Cys Leu Ser Cys Ile Thr Val Arg Ser
 645 650 655
 Phe Gln Ile Val Cys Val Phe Lys Met Ala Arg Arg Leu Pro Ser Ala
 660 665 670
 Tyr Ser Phe Trp Met Arg Tyr His Gly Pro Tyr Val Phe Val Ala Phe
 675 680 685
 Ile Thr Ala Ile Lys Val Ala Leu Val Val Gly Asn Met Leu Ala Thr
 690 695 700
 Thr Ile Asn Pro Ile Gly Arg Thr Asp Pro Asp Asp Pro Asn Ile Met
 705 710 715 720
 Ile Leu Ser Cys His Pro Asn Tyr Arg Asn Gly Leu Leu Phe Asn Thr
 725 730 735
 Ser Met Asp Leu Leu Leu Ser Val Leu Gly Phe Ser Phe Ala Tyr Met
 740 745 750
 Gly Lys Glu Leu Pro Thr Asn Tyr Asn Glu Ala Lys Phe Ile Thr Leu
 755 760 765
 Ser Met Thr Phe Ser Phe Thr Ser Ser Ile Ser Leu Cys Thr Phe Met
 770 775 780
 Ser Val His Asp Gly Val Leu Val Thr Ile Met Asp Leu Leu Val Thr
 785 790 795 800
 Val Leu Asn Phe Leu Ala Ile Gly Leu Gly Tyr Phe Gly Pro Lys Cys
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Tyr Met Ile Leu Phe Tyr Pro Glu Arg Asn Thr Ser Ala Tyr Phe Asn
820 825 830

Ser Met Ile Gln Gly Tyr Thr Met Arg Lys Ser
835 840

<210> 8

<211> 843

<212> PRT

<213> Mus musculus

<220>

<223> mouse T1R2 sweet taste receptor

<400> 8

Met Gly Pro Gln Ala Arg Thr Leu His Leu Leu Phe Leu Leu Leu His
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Ala Leu Pro Lys Pro Val Met Leu Val Gly Asn Ser Asp Phe His Leu
20 25 30

Ala Gly Asp Tyr Leu Leu Gly Gly Leu Phe Thr Leu His Ala Asn Val
35 40 45

Lys Ser Val Ser His Leu Ser Tyr Leu Gln Val Pro Lys Cys Asn Glu
50 55 60

Tyr Asn Met Lys Val Leu Gly Tyr Asn Leu Met Gln Ala Met Arg Phe
65 70 75 80

Ala Val Glu Glu Ile Asn Asn Cys Ser Ser Leu Leu Pro Gly Val Leu
85 90 95

Leu Gly Tyr Glu Met Val Asp Val Cys Tyr Leu Ser Asn Asn Ile Gln
100 105 110

Pro Gly Leu Tyr Phe Leu Ser Gln Ile Asp Asp Phe Leu Pro Ile Leu
115 120 125

Lys Asp Tyr Ser Gln Tyr Arg Pro Gln Val Val Ala Val Ile Gly Pro
130 135 140

Asp Asn Ser Glu Ser Ala Ile Thr Val Ser Asn Ile Leu Ser Tyr Phe
145 150 155 160

Leu Val Pro Gln Val Thr Tyr Ser Ala Ile Thr Asp Lys Leu Gln Asp
165 170 175

Lys Arg Arg Phe Pro Ala Met Leu Arg Thr Val Pro Ser Ala Thr His
180 185 190

His Ile Glu Ala Met Val Gln Leu Met Val His Phe Gln Trp Asn Trp
195 200 205

Ile Val Val Leu Val Ser Asp Asp Asp Tyr Gly Arg Glu Asn Ser His
210 215 220

Leu Leu Ser Gln Arg Leu Thr Asn Thr Gly Asp Ile Cys Ile Ala Phe
225 230 235 240

Gln Glu Val Leu Pro Val Pro Glu Pro Asn Gln Ala Val Arg Pro Glu
 245 250 255
 Glu Gln Asp Gln Leu Asp Asn Ile Leu Asp Lys Leu Arg Arg Thr Ser
 260 265 270
 Ala Arg Val Val Val Ile Phe Ser Pro Glu Leu Ser Leu His Asn Phe
 275 280 285
 Phe Arg Glu Val Leu Arg Trp Asn Phe Thr Gly Phe Val Trp Ile Ala
 290 295 300
 Ser Glu Ser Trp Ala Ile Asp Pro Val Leu His Asn Leu Thr Glu Leu
 305 310 315 320
 Arg His Thr Gly Thr Phe Leu Gly Val Thr Ile Gln Arg Val Ser Ile
 325 330 335
 Pro Gly Phe Ser Gln Phe Arg Val Arg His Asp Lys Pro Gly Tyr Arg
 340 345 350
 Met Pro Asn Glu Thr Ser Leu Arg Thr Thr Cys Asn Gln Asp Cys Asp
 355 360 365
 Ala Cys Met Asn Ile Thr Glu Ser Phe Asn Asn Val Leu Met Leu Ser
 370 375 380
 Gly Glu Arg Val Val Tyr Ser Val Tyr Ser Ala Val Tyr Ala Val Ala
 385 390 395 400
 His Thr Leu His Arg Leu Leu His Cys Asn Gln Val Arg Cys Thr Lys
 405 410 415
 Gln Ile Val Tyr Pro Trp Gln Leu Leu Arg Glu Ile Trp His Val Asn
 420 425 430
 Phe Thr Leu Leu Gly Asn Gln Leu Phe Phe Asp Glu Gln Gly Asp Met
 435 440 445
 Pro Met Leu Leu Asp Ile Ile Gln Trp Gln Trp Gly Leu Ser Gln Asn
 450 455 460
 Pro Phe Gln Ser Ile Ala Ser Tyr Ser Pro Thr Glu Thr Arg Leu Thr
 465 470 475 480
 Tyr Ile Ser Asn Val Ser Trp Tyr Thr Pro Asn Asn Thr Val Pro Ile
 485 490 495
 Ser Met Cys Ser Lys Ser Cys Gln Pro Gly Gln Met Lys Lys Pro Ile
 500 505 510
 Gly Leu His Pro Cys Cys Phe Glu Cys Val Asp Cys Pro Pro Asp Thr
 515 520 525
 Tyr Leu Asn Arg Ser Val Asp Glu Phe Asn Cys Leu Ser Cys Pro Gly
 530 535 540
 Ser Met Trp Ser Tyr Lys Asn Asn Ile Ala Cys Phe Lys Arg Arg Leu
 545 550 555 560

Ala Phe Leu Glu Trp His Glu Val Pro Thr Ile Val Val Thr Ile Leu
 565 570 575
 Ala Ala Leu Gly Phe Ile Ser Thr Leu Ala Ile Leu Leu Ile Phe Trp
 580 585 590
 Arg His Phe Gln Thr Pro Met Val Arg Ser Ala Gly Gly Pro Met Cys
 595 600 605
 Phe Leu Met Leu Val Pro Leu Leu Leu Ala Phe Gly Met Val Pro Val
 610 615 620
 Tyr Val Gly Pro Pro Thr Val Phe Ser Cys Phe Cys Arg Gln Ala Phe
 625 630 635 640
 Phe Thr Val Cys Phe Ser Val Cys Leu Ser Cys Ile Thr Val Arg Ser
 645 650 655
 Phe Gln Ile Val Cys Val Phe Lys Met Ala Arg Arg Leu Pro Ser Ala
 660 665 670
 Tyr Gly Phe Trp Met Arg Tyr His Gly Pro Tyr Val Phe Val Ala Phe
 675 680 685
 Ile Thr Ala Val Lys Val Ala Leu Val Ala Gly Asn Met Leu Ala Thr
 690 695 700
 Thr Ile Asn Pro Ile Gly Arg Thr Asp Pro Asp Asp Pro Asn Ile Ile
 705 710 715 720
 Ile Leu Ser Cys His Pro Asn Tyr Arg Asn Gly Leu Leu Phe Asn Thr
 725 730 735
 Ser Met Asp Leu Leu Leu Ser Val Leu Gly Phe Ser Phe Ala Tyr Val
 740 745 750
 Gly Lys Glu Leu Pro Thr Asn Tyr Asn Glu Ala Lys Phe Ile Thr Leu
 755 760 765
 Ser Met Thr Phe Ser Phe Thr Ser Ser Ile Ser Leu Cys Thr Phe Met
 770 775 780
 Ser Val His Asp Gly Val Leu Val Thr Ile Met Asp Leu Leu Val Thr
 785 790 795 800
 Val Leu Asn Phe Leu Ala Ile Gly Leu Gly Tyr Phe Gly Pro Lys Cys
 805 810 815
 Tyr Met Ile Leu Phe Tyr Pro Glu Arg Asn Thr Ser Ala Tyr Phe Asn
 820 825 830
 Ser Met Ile Gln Gly Tyr Thr Met Arg Lys Ser
 835 840

<210> 9
 <211> 838
 <212> PRT
 <213> Homo sapiens

<220>

<223> human T1R2 sweet taste receptor

<400> 9

Met Gly Pro Arg Ala Lys Thr Ile Cys Ser Leu Phe Phe Leu Leu Trp
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Tyr Leu Leu Gly Gly Leu Phe Ser Leu His Ala Asn Met Lys Gly Ile
35 40 45
Val His Leu Asn Phe Leu Gln Val Pro Met Cys Lys Glu Tyr Glu Val
50 55 60
Lys Val Ile Gly Tyr Asn Leu Met Gln Ala Met Arg Phe Ala Val Glu
65 70 75 80
Glu Ile Asn Asn Asp Ser Ser Leu Leu Pro Gly Val Leu Leu Gly Tyr
85 90 95
Glu Ile Val Asp Val Cys Tyr Ile Ser Asn Asn Val Gln Pro Val Leu
100 105 110
Tyr Phe Leu Ala His Glu Asp Asn Leu Leu Pro Ile Gln Glu Asp Tyr
115 120 125
Ser Asn Tyr Ile Ser Arg Val Val Ala Val Ile Gly Pro Asp Asn Ser
130 135 140
Glu Ser Val Met Thr Val Ala Asn Phe Leu Ser Leu Phe Leu Leu Pro
145 150 155 160
Gln Ile Thr Tyr Ser Ala Ile Ser Asp Glu Leu Arg Asp Lys Val Arg
165 170 175
Phe Pro Ala Leu Leu Arg Thr Thr Pro Ser Ala Asp His His Val Glu
180 185 190
Ala Met Val Gln Leu Met Leu His Phe Arg Trp Asn Trp Ile Ile Val
195 200 205
Leu Val Ser Ser Asp Thr Tyr Gly Arg Asp Asn Gly Gln Leu Leu Gly
210 215 220
Glu Arg Val Ala Arg Arg Asp Ile Cys Ile Ala Phe Gln Glu Thr Leu
225 230 235 240
Pro Thr Leu Gln Pro Asn Gln Asn Met Thr Ser Glu Glu Arg Gln Arg
245 250 255
Leu Val Thr Ile Val Asp Lys Leu Gln Gln Ser Thr Ala Arg Val Val
260 265 270
Val Val Phe Ser Pro Asp Leu Thr Leu Tyr His Phe Phe Asn Glu Val
275 280 285
Leu Arg Gln Asn Phe Thr Gly Ala Val Trp Ile Ala Ser Glu Ser Trp
290 295 300

Ala Ile Asp Pro Val Leu His Asn Leu Thr Glu Leu Gly His Leu Gly
 305 310 315 320
 Thr Phe Leu Gly Ile Thr Ile Gln Ser Val Pro Ile Pro Gly Phe Ser
 325 330 335
 Glu Phe Arg Glu Trp Gly Pro Gln Ala Gly Pro Pro Pro Leu Ser Arg
 340 345 350
 Thr Ser Gln Ser Tyr Thr Cys Asn Gln Glu Cys Asp Asn Cys Leu Asn
 355 360 365
 Ala Thr Leu Ser Phe Asn Thr Ile Leu Arg Leu Ser Gly Glu Arg Val
 370 375 380
 Val Tyr Ser Val Tyr Ser Ala Val Tyr Ala Val Ala His Ala Leu His
 385 390 395 400
 Ser Leu Leu Gly Cys Asp Lys Ser Thr Cys Thr Lys Arg Val Val Tyr
 405 410 415
 Pro Trp Gln Leu Leu Glu Glu Ile Trp Lys Val Asn Phe Thr Leu Leu
 420 425 430
 Asp His Gln Ile Phe Phe Asp Pro Gln Gly Asp Val Ala Leu His Leu
 435 440 445
 Glu Ile Val Gln Trp Gln Trp Asp Arg Ser Gln Asn Pro Phe Gln Ser
 450 455 460
 Val Ala Ser Tyr Tyr Pro Leu Gln Arg Gln Leu Lys Asn Ile Gln Asp
 465 470 475 480
 Ile Ser Trp His Thr Val Asn Asn Thr Ile Pro Met Ser Met Cys Ser
 485 490 495
 Lys Arg Cys Gln Ser Gly Gln Lys Lys Lys Pro Val Gly Ile His Val
 500 505 510
 Cys Cys Phe Glu Cys Ile Asp Cys Leu Pro Gly Thr Phe Leu Asn His
 515 520 525
 Thr Glu Asp Glu Tyr Glu Cys Gln Ala Cys Pro Asn Asn Glu Trp Ser
 530 535 540
 Tyr Gln Ser Glu Thr Ser Cys Phe Lys Arg Gln Leu Val Phe Leu Glu
 545 550 555 560
 Trp His Glu Ala Pro Thr Ile Ala Val Ala Leu Leu Ala Ala Leu Gly
 565 570 575
 Phe Leu Ser Thr Leu Ala Ile Leu Val Ile Phe Trp Arg His Phe Gln
 580 585 590
 Thr Pro Ile Val Arg Ser Ala Gly Gly Pro Met Cys Phe Leu Met Leu
 595 600 605
 Thr Leu Leu Leu Val Ala Tyr Met Val Val Pro Val Tyr Val Gly Pro
 610 615 620

Pro Lys Val Ser Thr Cys Leu Cys Arg Gln Ala Leu Phe Pro Leu Cys
 625 630 635 640
 Phe Thr Ile Cys Ile Ser Cys Ile Ala Val Arg Ser Phe Gln Ile Val
 645 650 655
 Cys Ala Phe Lys Met Ala Ser Arg Phe Pro Arg Ala Tyr Ser Tyr Trp
 660 665 670
 Val Arg Tyr Gln Gly Pro Tyr Val Ser Met Ala Phe Ile Thr Val Leu
 675 680 685
 Lys Met Val Ile Val Val Ile Gly Met Leu Ala Arg Pro Gln Ser His
 690 695 700
 Pro Arg Thr Asp Pro Asp Asp Pro Lys Ile Thr Ile Val Ser Cys Asn
 705 710 715 720
 Pro Asn Tyr Arg Asn Ser Leu Leu Phe Asn Thr Ser Leu Asp Leu Leu
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 Leu Ser Val Val Gly Phe Ser Phe Ala Tyr Met Gly Lys Glu Leu Pro
 740 745 750
 Thr Asn Tyr Asn Glu Ala Lys Phe Ile Thr Leu Ser Met Thr Phe Tyr
 755 760 765
 Phe Thr Ser Ser Val Ser Leu Cys Thr Phe Met Ser Ala Tyr Ser Gly
 770 775 780
 Val Leu Val Thr Ile Val Asp Leu Leu Val Thr Val Leu Asn Leu Leu
 785 790 795 800
 Ala Ile Ser Leu Gly Tyr Phe Gly Pro Lys Cys Tyr Met Ile Leu Phe
 805 810 815
 Tyr Pro Glu Arg Asn Thr Pro Ala Tyr Phe Asn Ser Met Ile Gln Gly
 820 825 830
 Tyr Thr Met Arg Arg Asp
 835

<210> 10

<211> 2993

<212> DNA

<213> Rattus sp.

<220>

<223> rat T1R2 sweet taste receptor

<400> 10

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 ctctctgggtg gcctctttac cctccatgcc aacgtgaaga gcatctccca cctcagctac 180
 ctgcaggtgc ccaagtgcaa tgagttcacc atgaaggtgt tgggctacaa cctcatgcag 240
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 cacgtgggtg ctgtcattgg ccccgacaac tctgagtcgg ccattaccgt gtccaacatt 480
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<212> DNA

<213> Homo sapiens

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<223> human T1R2 sweet taste receptor

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 <211> 852
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human T1R3 sweet taste receptor

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Gly Asp Tyr Val Leu Gly Gly Leu Phe Pro Leu Gly Glu Ala Glu Glu
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Ala Gly Leu Arg Ser Arg Thr Arg Pro Ser Ser Pro Val Cys Thr Arg
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Phe Ser Ser Asn Gly Leu Leu Trp Ala Leu Ala Met Lys Met Ala Val
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Glu Glu Ile Asn Asn Lys Ser Asp Leu Leu Pro Gly Leu Arg Leu Gly
          85                      90                      95

Tyr Asp Leu Phe Asp Thr Cys Ser Glu Pro Val Val Ala Met Lys Pro
          100                      105                      110

Ser Leu Met Phe Leu Ala Lys Ala Gly Ser Arg Asp Ile Ala Ala Tyr
          115                      120                      125

Cys Asn Tyr Thr Gln Tyr Gln Pro Arg Val Leu Ala Val Ile Gly Pro
          130                      135                      140

His Ser Ser Glu Leu Ala Met Val Thr Gly Lys Phe Phe Ser Phe Phe
          145                      150                      155                      160

Leu Met Pro Gln Val Ser Tyr Gly Ala Ser Met Glu Leu Leu Ser Ala
          165                      170                      175

Arg Glu Thr Phe Pro Ser Phe Phe Arg Thr Val Pro Ser Asp Arg Val
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Ile	Phe	Ser	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Ile	Cys	Ile	Ala	His	Glu		
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Gly	Leu	Val	Pro	Leu	Pro	Arg	Ala	Asp	Asp	Ser	Arg	Leu	Gly	Lys	Val		
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Tyr	Val	Lys	Thr	His	Leu	Ala	Leu	Ala	Thr	Asp	Pro	Ala	Phe	Cys	Ser		
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Arg	Cys	Pro	Gln	Cys	Asp	Cys	Ile	Thr	Leu	Gln	Asn	Val	Ser	Ala	Gly		
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 Glu Trp Ser Pro Glu Arg Ser Thr Arg Cys Phe Arg Arg Arg Ser Arg
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 580 585 590
 His Arg Asp Ser Pro Leu Val Gln Ala Ser Gly Gly Pro Leu Ala Cys
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 Phe Gly Leu Val Cys Leu Gly Leu Val Cys Leu Ser Val Leu Leu Phe
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 Pro Gly Gln Pro Ser Pro Ala Arg Cys Leu Ala Gln Gln Pro Leu Ser
 625 630 635 640
 His Leu Pro Leu Thr Gly Cys Leu Ser Thr Leu Phe Leu Gln Ala Ala
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 Glu Ile Phe Val Glu Ser Glu Leu Pro Leu Ser Trp Ala Asp Arg Leu
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 Ser Gly Cys Leu Arg Gly Pro Trp Ala Trp Leu Val Val Leu Leu Ala
 675 680 685
 Met Leu Val Glu Val Ala Leu Cys Thr Trp Tyr Leu Val Ala Phe Pro
 690 695 700
 Pro Glu Val Val Thr Asp Trp His Met Leu Pro Thr Glu Ala Leu Val
 705 710 715 720
 His Cys Arg Thr Arg Ser Trp Val Ser Phe Gly Leu Ala His Ala Thr
 725 730 735
 Asn Ala Thr Leu Ala Phe Leu Cys Phe Leu Gly Thr Phe Leu Val Arg
 740 745 750
 Ser Gln Pro Gly Cys Tyr Asn Arg Ala Arg Gly Leu Thr Phe Ala Met
 755 760 765
 Leu Ala Tyr Phe Ile Thr Trp Val Ser Phe Val Pro Leu Leu Ala Asn
 770 775 780
 Val Gln Val Val Leu Arg Pro Ala Val Gln Met Gly Ala Leu Leu Leu
 785 790 795 800
 Cys Val Leu Gly Ile Leu Ala Ala Phe His Leu Pro Arg Cys Tyr Leu
 805 810 815
 Leu Met Arg Gln Pro Gly Leu Asn Thr Pro Glu Phe Phe Leu Gly Gly
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Gly Pro Gly Asp Ala Gln Gly Gln Asn Asp Gly Asn Thr Gly Asn Gln
835 840 845

Gly Lys His Glu
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<210> 16
<211> 3240
<212> DNA
<213> Mus musculus

<220>
<223> mouse Sac non taster 129 T1R3 sweet taste receptor
genomic

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<210> 17

<211> 2577

<212> DNA

<213> Mus musculus

<220>

<223> mouse Sac non taster 129 T1R3 sweet taste receptor
CDS

<400> 17

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<210> 18
 <211> 858
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<220>
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 Gly Asp Tyr Ile Leu Gly Gly Leu Phe Pro Leu Gly Ser Thr Glu Glu
 35 40 45
 Ala Thr Leu Asn Gln Arg Ala Gln Pro Asn Ser Thr Leu Cys Asn Arg
 50 55 60
 Phe Ser Pro Leu Gly Leu Phe Leu Ala Met Ala Met Lys Met Ala Val
 65 70 75 80
 Glu Glu Ile Asn Asn Gly Ser Ala Leu Leu Pro Gly Leu Arg Leu Gly
 85 90 95
 Tyr Asp Leu Phe Asp Thr Cys Ser Glu Pro Val Val Thr Met Lys Ser
 100 105 110
 Ser Leu Met Phe Leu Ala Lys Val Gly Ser Gln Ser Ile Ala Ala Tyr
 115 120 125
 Cys Asn Tyr Thr Gln Tyr Gln Pro Arg Val Leu Ala Val Ile Gly Pro
 130 135 140
 His Ser Ser Glu Leu Ala Leu Ile Thr Gly Lys Phe Phe Ser Phe Phe
 145 150 155 160
 Leu Met Pro Gln Val Ser Tyr Ser Ala Ser Met Asp Arg Leu Ser Asp
 165 170 175
 Arg Glu Thr Phe Pro Ser Phe Phe Arg Thr Val Pro Ser Asp Arg Val
 180 185 190
 Gln Leu Gln Ala Val Val Thr Leu Leu Gln Asn Phe Ser Trp Asn Trp
 195 200 205
 Val Ala Ala Leu Gly Ser Asp Asp Asp Tyr Gly Arg Glu Gly Leu Ser
 210 215 220
 Ile Phe Ser Ser Leu Ala Asn Ala Arg Gly Ile Cys Ile Ala His Glu
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Gly	Leu	Val	Pro	Gln	His	Asp	Thr	Ser	Gly	Gln	Gln	Leu	Gly	Lys	Val	
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Leu	Asp	Val	Leu	Arg	Gln	Val	Asn	Gln	Ser	Lys	Val	Gln	Val	Val	Val	
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 595 600 605
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 Gln Gln Pro Met Ala His Leu Pro Leu Thr Gly Cys Leu Ser Thr Leu
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 675 680 685
 Val Val Leu Leu Ala Thr Phe Val Glu Ala Ala Leu Cys Ala Trp Tyr
 690 695 700
 Leu Thr Ala Phe Pro Pro Glu Val Val Thr Asp Trp Ser Val Leu Pro
 705 710 715 720
 Thr Glu Val Leu Glu His Cys His Val Arg Ser Trp Val Ser Leu Gly
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 Leu Val His Ile Thr Asn Ala Met Leu Ala Phe Leu Cys Phe Leu Gly
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 755 760 765
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 785 790 795 800
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<210> 19
 <211> 2577
 <212> DNA
 <213> Mus musculus

<220>
 <223> mouse Sac taster SWR T1R3 sweet taste receptor CDS

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 <212> PRT
 <213> Mus musculus

<220>
 <223> mouse Sac taster SWR T1R3 sweet taste receptor

<400> 20

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Gly Asp Tyr Ile Leu Gly Gly Leu Phe Pro Leu Gly Ser Thr Glu Glu
35 40 45
Ala Thr Leu Asn Gln Arg Thr Gln Pro Asn Ser Ile Leu Cys Asn Arg
50 55 60
Phe Ser Pro Leu Gly Leu Phe Leu Ala Met Ala Met Lys Met Ala Val
65 70 75 80
Glu Glu Ile Asn Asn Gly Ser Ala Leu Leu Pro Gly Leu Arg Leu Gly
85 90 95
Tyr Asp Leu Phe Asp Thr Cys Ser Glu Pro Val Val Thr Met Lys Ser
100 105 110
Ser Leu Met Phe Leu Ala Lys Val Gly Ser Gln Ser Ile Ala Ala Tyr
115 120 125
Cys Asn Tyr Thr Gln Tyr Gln Pro Arg Val Leu Ala Val Ile Gly Pro
130 135 140
His Ser Ser Glu Leu Ala Leu Ile Thr Gly Lys Phe Phe Ser Phe Phe
145 150 155 160
Leu Met Pro Gln Val Ser Tyr Ser Ala Ser Met Asp Arg Leu Ser Asp
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Arg Glu Thr Phe Pro Ser Phe Phe Arg Thr Val Pro Ser Asp Arg Val
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Gln Leu Gln Ala Val Val Thr Leu Leu Gln Asn Phe Ser Trp Asn Trp
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Val Ala Ala Leu Gly Ser Asp Asp Tyr Gly Arg Glu Gly Leu Ser
210 215 220
Ile Phe Ser Ser Leu Ala Asn Ala Arg Gly Ile Cys Ile Ala His Glu
225 230 235 240
Gly Leu Val Pro Gln His Asp Thr Ser Gly Gln Gln Leu Gly Lys Val
245 250 255
Leu Asp Val Leu Cys Gln Val Asn Gln Ser Lys Val Gln Val Val Val
260 265 270
Leu Phe Ala Ser Ala Arg Ala Val Tyr Ser Leu Phe Ser Tyr Ser Ile
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His His Gly Leu Ser Pro Lys Val Trp Val Ala Ser Glu Ser Trp Leu
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Thr Ser Asp Leu Val Met Thr Leu Pro Asn Ile Ala Arg Val Gly Thr
305 310 315 320

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Tyr Val Glu Thr His Leu Ala Leu Ala Ala Asp Pro Ala Phe Cys Ala
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Cys Pro Gln Cys Asp Asp Ile Met Leu Gln Asn Leu Ser Ser Gly Leu
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Leu Gln Asn Leu Ser Ala Gly Gln Leu His His Gln Ile Phe Ala Thr
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Tyr Ala Ala Val Tyr Ser Val Ala Gln Ala Leu His Asn Thr Leu Gln
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Cys Asn Val Ser His Cys His Val Ser Glu His Val Leu Pro Trp Gln
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Leu Leu Glu Asn Met Tyr Asn Met Ser Phe His Ala Arg Asp Leu Thr
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Leu Gln Phe Asp Ala Glu Gly Asn Val Asp Met Glu Tyr Asp Leu Lys
450 455 460
Met Trp Val Trp Gln Ser Pro Thr Pro Val Leu His Thr Val Gly Thr
465 470 475 480
Phe Asn Gly Thr Leu Gln Leu Gln Gln Ser Lys Met Tyr Trp Pro Gly
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Asn Gln Val Pro Val Ser Gln Cys Ser Arg Gln Cys Lys Asp Gly Gln
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Cys Lys Ala Gly Ser Tyr Arg Lys His Pro Asp Asp Phe Thr Cys Thr
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 785 790 795 800
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 805 810 815
 Pro Lys Cys Tyr Val Leu Leu Trp Leu Pro Lys Leu Asn Thr Gln Glu
 820 825 830
 Phe Phe Leu Gly Arg Asn Ala Lys Lys Ala Ala Asp Glu Asn Ser Gly
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<210> 21

<211> 3200

<212> DNA

<213> Mus musculus

<220>

<223> mouse Sac taster C57 T1R3 sweet taste receptor
genomic

<400> 21

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<210> 22

<211> 2577

<212> DNA

<213> Mus musculus

<220>

<223> mouse Sac taster C57 T1R3 sweet taste receptor CDS

<400> 22

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<210> 23

<211> 858

<212> PRT

<213> Mus musculus

<220>

<223> mouse Sac taster C57 T1R3 sweet taste receptor

<400> 23

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			20						25				30		

Gly	Asp	Tyr	Ile	Leu	Gly	Gly	Leu	Phe	Pro	Leu	Gly	Ser	Thr	Glu	Glu
		35					40					45			

Ala	Thr	Leu	Asn	Gln	Arg	Thr	Gln	Pro	Asn	Ser	Ile	Pro	Cys	Asn	Arg
	50						55				60				

Phe	Ser	Pro	Leu	Gly	Leu	Phe	Leu	Ala	Met	Ala	Met	Lys	Met	Ala	Val	65	70	75	80
Glu	Glu	Ile	Asn	Asn	Gly	Ser	Ala	Leu	Leu	Pro	Gly	Leu	Arg	Leu	Gly		85	90	95
Tyr	Asp	Leu	Phe	Asp	Thr	Cys	Ser	Glu	Pro	Val	Val	Thr	Met	Lys	Ser	100	105	110	
Ser	Leu	Met	Phe	Leu	Ala	Lys	Val	Gly	Ser	Gln	Ser	Ile	Ala	Ala	Tyr	115	120	125	
Cys	Asn	Tyr	Thr	Gln	Tyr	Gln	Pro	Arg	Val	Leu	Ala	Val	Ile	Gly	Pro	130	135	140	
His	Ser	Ser	Glu	Leu	Ala	Leu	Ile	Thr	Gly	Lys	Phe	Phe	Ser	Phe	Phe	145	150	155	160
Leu	Met	Pro	Gln	Val	Ser	Tyr	Ser	Ala	Ser	Met	Asp	Arg	Leu	Ser	Asp	165	170		175
Arg	Glu	Thr	Phe	Pro	Ser	Phe	Phe	Arg	Thr	Val	Pro	Ser	Asp	Arg	Val	180	185	190	
Gln	Leu	Gln	Ala	Val	Val	Thr	Leu	Leu	Gln	Asn	Phe	Ser	Trp	Asn	Trp	195	200	205	
Val	Ala	Ala	Leu	Gly	Ser	Asp	Asp	Asp	Tyr	Gly	Arg	Glu	Gly	Leu	Ser	210	215	220	
Ile	Phe	Ser	Ser	Leu	Ala	Asn	Ala	Arg	Gly	Ile	Cys	Ile	Ala	His	Glu	225	230	235	240
Gly	Leu	Val	Pro	Gln	His	Asp	Thr	Ser	Gly	Gln	Gln	Leu	Gly	Lys	Val	245	250	255	
Leu	Asp	Val	Leu	Arg	Gln	Val	Asn	Gln	Ser	Lys	Val	Gln	Val	Val	Val	260	265	270	
Leu	Phe	Ala	Ser	Ala	Arg	Ala	Val	Tyr	Ser	Leu	Phe	Ser	Tyr	Ser	Ile	275	280	285	
His	His	Gly	Leu	Ser	Pro	Lys	Val	Trp	Val	Ala	Ser	Glu	Ser	Trp	Leu	290	295	300	
Thr	Ser	Asp	Leu	Val	Met	Thr	Leu	Pro	Asn	Ile	Ala	Arg	Val	Gly	Thr	305	310	315	320
Val	Leu	Gly	Phe	Leu	Gln	Arg	Gly	Ala	Leu	Leu	Pro	Glu	Phe	Ser	His	325	330	335	
Tyr	Val	Glu	Thr	His	Leu	Ala	Leu	Ala	Ala	Asp	Pro	Ala	Phe	Cys	Ala	340	345	350	
Ser	Leu	Asn	Ala	Glu	Leu	Asp	Leu	Glu	Glu	His	Val	Met	Gly	Gln	Arg	355	360	365	
Cys	Pro	Arg	Cys	Asp	Asp	Ile	Met	Leu	Gln	Asn	Leu	Ser	Ser	Gly	Leu	370	375	380	

Leu	Gln	Asn	Leu	Ser	Ala	Gly	Gln	Leu	His	His	Gln	Ile	Phe	Ala	Thr	
385					390					395					400	
Tyr	Ala	Ala	Val	Tyr	Ser	Val	Ala	Gln	Ala	Leu	His	Asn	Thr	Leu	Gln	
				405					410					415		
Cys	Asn	Val	Ser	His	Cys	His	Val	Ser	Glu	His	Val	Leu	Pro	Trp	Gln	
			420					425					430			
Leu	Leu	Glu	Asn	Met	Tyr	Asn	Met	Ser	Phe	His	Ala	Arg	Asp	Leu	Thr	
		435					440					445				
Leu	Gln	Phe	Asp	Ala	Glu	Gly	Asn	Val	Asp	Met	Glu	Tyr	Asp	Leu	Lys	
	450					455					460					
Met	Trp	Val	Trp	Gln	Ser	Pro	Thr	Pro	Val	Leu	His	Thr	Val	Gly	Thr	
465					470					475					480	
Phe	Asn	Gly	Thr	Leu	Gln	Leu	Gln	Gln	Ser	Lys	Met	Tyr	Trp	Pro	Gly	
				485					490					495		
Asn	Gln	Val	Pro	Val	Ser	Gln	Cys	Ser	Arg	Gln	Cys	Lys	Asp	Gly	Gln	
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Val	Arg	Arg	Val	Lys	Gly	Phe	His	Ser	Cys	Cys	Tyr	Asp	Cys	Val	Asp	
			515				520					525				
Cys	Lys	Ala	Gly	Ser	Tyr	Arg	Lys	His	Pro	Asp	Asp	Phe	Thr	Cys	Thr	
	530					535					540					
Pro	Cys	Asn	Gln	Asp	Gln	Trp	Ser	Pro	Glu	Lys	Ser	Thr	Ala	Cys	Leu	
545					550					555					560	
Pro	Arg	Arg	Pro	Lys	Phe	Leu	Ala	Trp	Gly	Glu	Pro	Val	Val	Leu	Ser	
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Leu	Leu	Leu	Leu	Leu	Cys	Leu	Val	Leu	Gly	Leu	Ala	Leu	Ala	Ala	Leu	
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Gly	Leu	Ser	Val	His	His	Trp	Asp	Ser	Pro	Leu	Val	Gln	Ala	Ser	Gly	
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	610					615					620					
Ser	Val	Leu	Leu	Phe	Pro	Gly	Arg	Pro	Ser	Ser	Ala	Ser	Cys	Leu	Ala	
625					630					635					640	
Gln	Gln	Pro	Met	Ala	His	Leu	Pro	Leu	Thr	Gly	Cys	Leu	Ser	Thr	Leu	
				645					650					655		
Phe	Leu	Gln	Ala	Ala	Glu	Thr	Phe	Val	Glu	Ser	Glu	Leu	Pro	Leu	Ser	
			660					665					670			
Trp	Ala	Asn	Trp	Leu	Cys	Ser	Tyr	Leu	Arg	Gly	Leu	Trp	Ala	Trp	Leu	
		675					680					685				
Val	Val	Leu	Leu	Ala	Thr	Phe	Val	Glu	Ala	Ala	Leu	Cys	Ala	Trp	Tyr	
	690					695					700					

Leu Ile Ala Phe Pro Pro Glu Val Val Thr Asp Trp Ser Val Leu Pro
 705 710 715 720
 Thr Glu Val Leu Glu His Cys His Val Arg Ser Trp Val Ser Leu Gly
 725 730 735
 Leu Val His Ile Thr Asn Ala Met Leu Ala Phe Leu Cys Phe Leu Gly
 740 745 750
 Thr Phe Leu Val Gln Ser Gln Pro Gly Arg Tyr Asn Arg Ala Arg Gly
 755 760 765
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 770 775 780
 Pro Leu Leu Ala Asn Val Gln Val Ala Tyr Gln Pro Ala Val Gln Met
 785 790 795 800
 Gly Ala Ile Leu Val Cys Ala Leu Gly Ile Leu Val Thr Phe His Leu
 805 810 815
 Pro Lys Cys Tyr Val Leu Leu Trp Leu Pro Lys Leu Asn Thr Gln Glu
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 850 855

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 <213> Rattus sp.

<220>
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<211> 858

<212> PRT

<213> Rattus sp.

<220>

<223> rat T1R3 sweet taste receptor

<400> 25

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  1                      5                      10                      15

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Leu Gly Met Gly Ser Ser Leu Cys Leu Ser Gln Gln Phe Lys Ala Gln
          20                      25                      30

```

```

Gly Asp Tyr Ile Leu Gly Gly Leu Phe Pro Leu Gly Thr Thr Glu Glu
          35                      40                      45

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```

Ala Thr Leu Asn Gln Arg Thr Gln Pro Asn Gly Ile Leu Cys Thr Arg
          50                      55                      60

```

```

Phe Ser Pro Leu Gly Leu Phe Leu Ala Met Ala Met Lys Met Ala Val
          65                      70                      75                      80

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```

Glu Glu Ile Asn Asn Gly Ser Ala Leu Leu Pro Gly Leu Arg Leu Gly
          85                      90                      95

```

```

Tyr Asp Leu Phe Asp Thr Cys Ser Glu Pro Val Val Thr Met Lys Pro
          100                     105                     110

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Ser Leu Met Phe Met Ala Lys Val Gly Ser Gln Ser Ile Ala Ala Tyr
          115                     120                     125

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Cys Asn Tyr Thr Gln Tyr Gln Pro Arg Val Leu Ala Val Ile Gly Pro
          130                     135                     140

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His Ser Ser Glu Leu Ala Leu Ile Thr Gly Lys Phe Phe Ser Phe Phe
 145 150 155 160
 Leu Met Pro Gln Val Ser Tyr Ser Ala Ser Met Asp Arg Leu Ser Asp
 165 170 175
 Arg Glu Thr Phe Pro Ser Phe Phe Arg Thr Val Pro Ser Asp Arg Val
 180 185 190
 Gln Leu Gln Ala Val Val Thr Leu Leu Gln Asn Phe Ser Trp Asn Trp
 195 200 205
 Val Ala Ala Leu Gly Ser Asp Asp Asp Tyr Gly Arg Glu Gly Leu Ser
 210 215 220
 Ile Phe Ser Gly Leu Ala Asn Ser Arg Gly Ile Cys Ile Ala His Glu
 225 230 235 240
 Gly Leu Val Pro Gln His Asp Thr Ser Gly Gln Gln Leu Gly Lys Val
 245 250 255
 Val Asp Val Leu Arg Gln Val Asn Gln Ser Lys Val Gln Val Val Val
 260 265 270
 Leu Phe Ala Ser Ala Arg Ala Val Tyr Ser Leu Phe Ser Tyr Ser Ile
 275 280 285
 Leu His Asp Leu Ser Pro Lys Val Trp Val Ala Ser Glu Ser Trp Leu
 290 295 300
 Thr Ser Asp Leu Val Met Thr Leu Pro Asn Ile Ala Arg Val Gly Thr
 305 310 315 320
 Val Leu Gly Phe Leu Gln Arg Gly Ala Leu Leu Pro Glu Phe Ser His
 325 330 335
 Tyr Val Glu Thr Arg Leu Ala Leu Ala Ala Asp Pro Thr Phe Cys Ala
 340 345 350
 Ser Leu Lys Ala Glu Leu Asp Leu Glu Glu Arg Val Met Gly Pro Arg
 355 360 365
 Cys Ser Gln Cys Asp Tyr Ile Met Leu Gln Asn Leu Ser Ser Gly Leu
 370 375 380
 Met Gln Asn Leu Ser Ala Gly Gln Leu His His Gln Ile Phe Ala Thr
 385 390 395 400
 Tyr Ala Ala Val Tyr Ser Val Ala Gln Ala Leu His Asn Thr Leu Gln
 405 410 415
 Cys Asn Val Ser His Cys His Thr Ser Glu Pro Val Gln Pro Trp Gln
 420 425 430
 Leu Leu Glu Asn Met Tyr Asn Met Ser Phe Arg Ala Arg Asp Leu Thr
 435 440 445
 Leu Gln Phe Asp Ala Lys Gly Ser Val Asp Met Glu Tyr Asp Leu Lys
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Met	Trp	Val	Trp	Gln	Ser	Pro	Thr	Pro	Val	Leu	His	Thr	Val	Gly	Thr	465	470	475	480
Phe	Asn	Gly	Thr	Leu	Gln	Leu	Gln	His	Ser	Lys	Met	Tyr	Trp	Pro	Gly	485	490	495	
Asn	Gln	Val	Pro	Val	Ser	Gln	Cys	Ser	Arg	Gln	Cys	Lys	Asp	Gly	Gln	500	505	510	
Val	Arg	Arg	Val	Lys	Gly	Phe	His	Ser	Cys	Cys	Tyr	Asp	Cys	Val	Asp	515	520	525	
Cys	Lys	Ala	Gly	Ser	Tyr	Arg	Lys	His	Pro	Asp	Asp	Phe	Thr	Cys	Thr	530	535	540	
Pro	Cys	Gly	Lys	Asp	Gln	Trp	Ser	Pro	Glu	Lys	Ser	Thr	Thr	Cys	Leu	545	550	555	560
Pro	Arg	Arg	Pro	Lys	Phe	Leu	Ala	Trp	Gly	Glu	Pro	Ala	Val	Leu	Ser	565	570		575
Leu	Leu	Leu	Leu	Leu	Cys	Leu	Val	Leu	Gly	Leu	Thr	Leu	Ala	Ala	Leu	580	585		590
Gly	Leu	Phe	Val	His	Tyr	Trp	Asp	Ser	Pro	Leu	Val	Gln	Ala	Ser	Gly	595	600	605	
Gly	Ser	Leu	Phe	Cys	Phe	Gly	Leu	Ile	Cys	Leu	Gly	Leu	Phe	Cys	Leu	610	615	620	
Ser	Val	Leu	Leu	Phe	Pro	Gly	Arg	Pro	Arg	Ser	Ala	Ser	Cys	Leu	Ala	625	630	635	640
Gln	Gln	Pro	Met	Ala	His	Leu	Pro	Leu	Thr	Gly	Cys	Leu	Ser	Thr	Leu	645	650		655
Phe	Leu	Gln	Ala	Ala	Glu	Ile	Phe	Val	Glu	Ser	Glu	Leu	Pro	Leu	Ser	660	665		670
Trp	Ala	Asn	Trp	Leu	Cys	Ser	Tyr	Leu	Arg	Gly	Pro	Trp	Ala	Trp	Leu	675	680	685	
Val	Val	Leu	Leu	Ala	Thr	Leu	Val	Glu	Ala	Ala	Leu	Cys	Ala	Trp	Tyr	690	695	700	
Leu	Met	Ala	Phe	Pro	Pro	Glu	Val	Val	Thr	Asp	Trp	Gln	Val	Leu	Pro	705	710	715	720
Thr	Glu	Val	Leu	Glu	His	Cys	Arg	Met	Arg	Ser	Trp	Val	Ser	Leu	Gly	725	730		735
Leu	Val	His	Ile	Thr	Asn	Ala	Val	Leu	Ala	Phe	Leu	Cys	Phe	Leu	Gly	740	745		750
Thr	Phe	Leu	Val	Gln	Ser	Gln	Pro	Gly	Arg	Tyr	Asn	Arg	Ala	Arg	Gly	755	760	765	
Leu	Thr	Phe	Ala	Met	Leu	Ala	Tyr	Phe	Ile	Ile	Trp	Val	Ser	Phe	Val	770	775	780	

Pro	Leu	Leu	Ala	Asn	Val	Gln	Val	Ala	Tyr	Gln	Pro	Ala	Val	Gln	Met
785					790					795					800
Gly	Ala	Ile	Leu	Phe	Cys	Ala	Leu	Gly	Ile	Leu	Ala	Thr	Phe	His	Leu
				805					810					815	
Pro	Lys	Cys	Tyr	Val	Leu	Leu	Trp	Leu	Pro	Glu	Leu	Asn	Thr	Gln	Glu
			820					825					830		
Phe	Phe	Leu	Gly	Arg	Ser	Pro	Lys	Glu	Ala	Ser	Asp	Gly	Asn	Ser	Gly
		835					840					845			
Ser	Ser	Glu	Ala	Thr	Arg	Gly	His	Ser	Glu						
850						855									